qiime2 Platform

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An Introduction to QIIME2

- Cancer and the microbiome
- What is QIIME2?
- QIIME2 Core Installation
- Tools for reproducibility and visualization
- Showcase of core methods and visualizations
- Community Support
- Workshops and tutorials
- The future of QIIME2

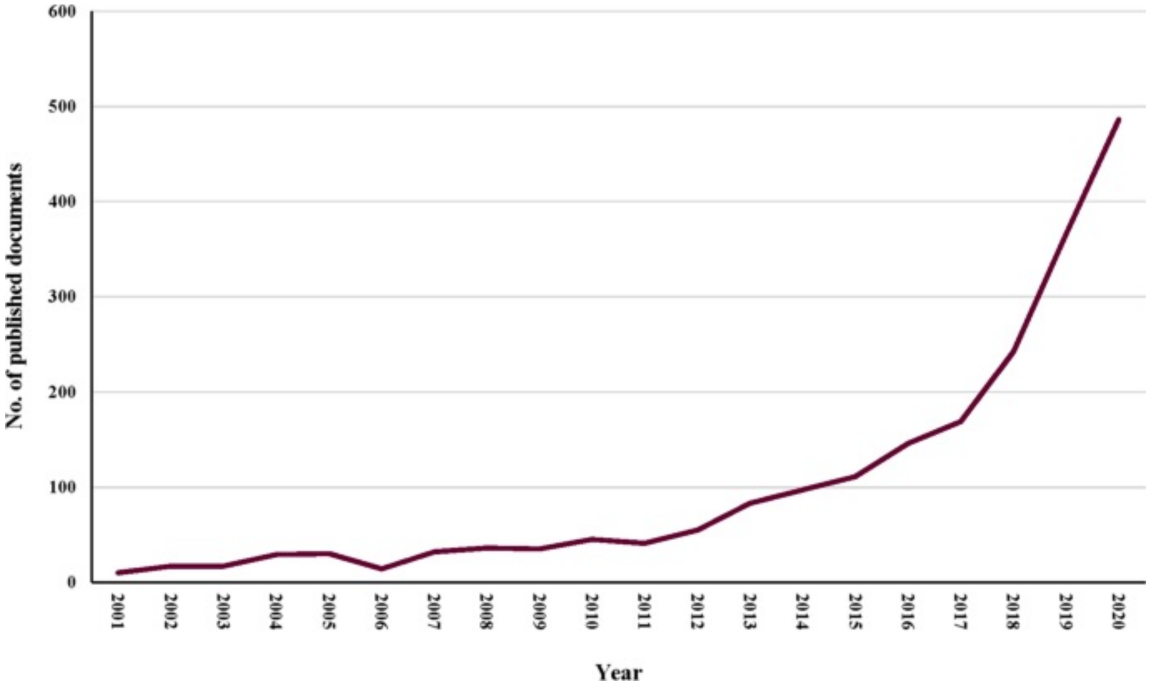
Trends in Microbiome Research

Microbiome – a collection or community of microorganisms in a defined environment

https://www.google.com/imgres?imgurl=https%3A%2F%2Fhips.hearstapps.com%2Fhmg-prod.s3.amazonaws.com%2Fimages%2F981%2Farticles%2F2015%2F09%2Fsoil-in-hands-francesca-yorke-1524578402.jpg%3Fcrop%3D1xw%3A0.884xh%3Bcenter%2Ctop%26resize%3D1200%3A*&imgrefurl=https%3A%2F%2Fwww.goodhousekeeping.com%2Fhome%2Fgardening%2Fa20705682%2Fsoil-testing%2F&tbnid=x8GwsXj_5W3r4M&vet=12ahU
5sZM&w=1100&h=550&q=soil&hl=en&ved=2ahU

https://www.google.com/imgres?imgurl=https%3A%2F%2Fassets.weforum.org%2Farticle%2Fimage%2FLrvg8rLmEzB5wfaPlpI02EZbCLvslFwLENLoANfrsJw.jpg&imgrefurl=https%3A%2F%2Fwww.weforum.org%2Fagenda%2F2021%2F01%2Fif-you-want-to-make-progress-on-all-the-major-global-challenges-start-with-
UIARDnAQ..i&docid=5SWgA
DcQQMygKegUIARDnAQ

https://www.science.org/content/webinar/your-microbiota-and-you-exploring-host-microbiome-relationship-health-and-disease



Growth trends of publications on the microbiota and cancer from 2001 to 2020, Zyoud et al. 2022, *Journal of Translational Medicine*

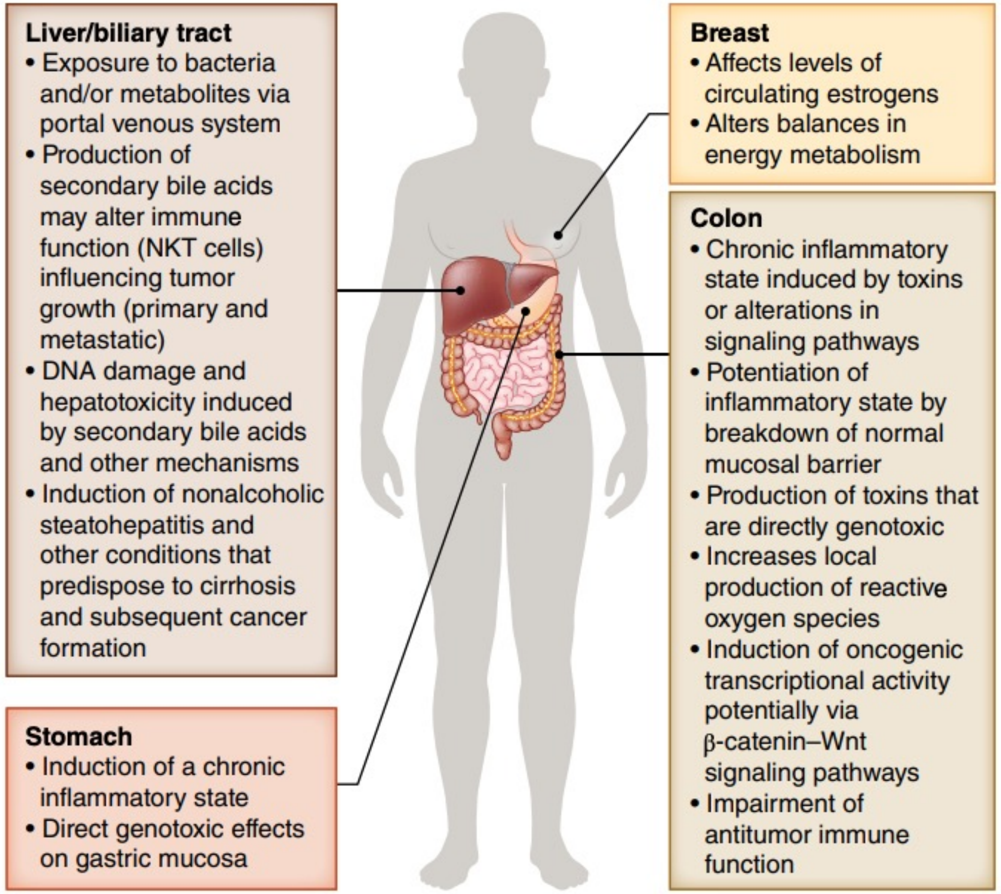
The role of the microbiome in cancer

The microbiome, cancer, and cancer therapy

Beth A. Helmink, M. A. Wadud Khan, Amanda Hermann, Vancheswaran Gopalakrishnan & Jennifer A. Wargo

Nature Medicine **25**, 377–388 (2019) | Cite this article

52k Accesses | **321** Citations | **240** Altmetric | Metrics



Liver/biliary tract
- Exposure to bacteria and/or metabolites via portal venous system
- Production of secondary bile acids may alter immune function (NKT cells) influencing tumor growth (primary and metastatic)
- DNA damage and hepatotoxicity induced by secondary bile acids and other mechanisms
- Induction of nonalcoholic steatohepatitis and other conditions that predispose to cirrhosis and subsequent cancer formation

Stomach
- Induction of a chronic inflammatory state
- Direct genotoxic effects on gastric mucosa

Breast
- Affects levels of circulating estrogens
- Alters balances in energy metabolism

Colon
- Chronic inflammatory state induced by toxins or alterations in signaling pathways
- Potentiation of inflammatory state by breakdown of normal mucosal barrier
- Production of toxins that are directly genotoxic
- Increases local production of reactive oxygen species
- Induction of oncogenic transcriptional activity potentially via β-catenin–Wnt signaling pathways
- Impairment of antitumor immune function

Fig. 1 | The influence of gut microbiota on cancer development. Shown are various mechanisms through which dysbiosis is proposed to affect tumorigenesis and/or tumor growth across cancer types, including colon, hepatobiliary, gastric and breast. Credit: Debbie Maizels/Springer Nature.

The role of the microbiome in cancer

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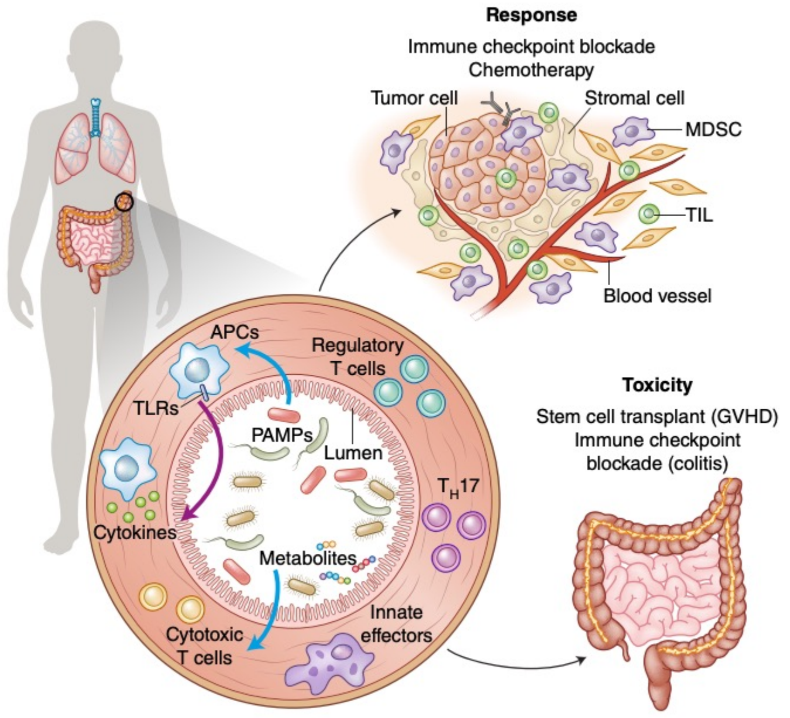


Fig. 2 | The influence of the gut microbiota on different cancer therapies. Gut microbes can impact both the response to various cancer therapies and associated toxicities, such as colitis and GVHD. The gut microbiota is thought to alter systemic immune function via local changes within the gut mucosa and gut-associated lymphoid tissue. The interaction of PAMPs with APCs and innate effectors via PRRs (TLRs) can help prime an adaptive immune response. Cytokines and microbial metabolites produced locally can act systemically. These combined activities lead to increased antitumor immune function with increased numbers of tumor-infiltrating lymphocytes (TILs) and decreased numbers of myeloid-derived suppressor cells (MDSCs). Credit: Debbie Maizels/Springer Nature.

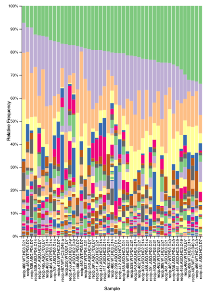
Basic steps in a microbiome analysis

Sample Collection / Wet lab work

Raw Sequencing Data

>NR_024570.1 Escherichia coli strain U 5/41 16S ribosomal RNA, partial sequence
AGTTTGATCATGGCTCAGATTGAACGCT
GGCGGCAGGCCTAACACATGCAAGTCG
AACGGTAACAGGAAG
CAGCTTGCTGCTTTGCTGACGAGTGGCG
GACGGGTGAGTAATGTCTGGGAAACTG
CCTGATGGAGGGGGA……

Statistical Results / Visualizations



16S rRNA = Bacteria / Archaea
18S rRNA = microbial eukaryotes
ITS = Fungi

Sequencing

Quality control

Clustering / Denoising

Normalization, Diversity Assessments

qiime2

Differential Abundance Testing

Sample Classification: RF

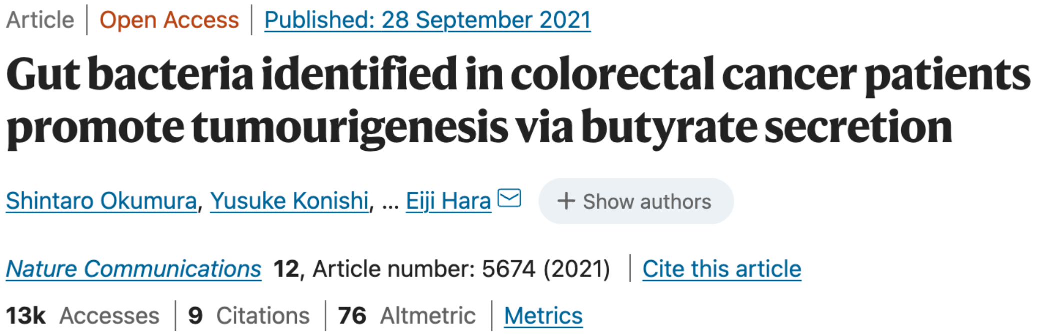
Longitudinal Analysis

Sequence Processing / Analysis

What is QIIME2?

A powerful, extensible, and decentralized microbiome analysis package with a focus on data and analysis transparency. QIIME 2 enables researchers to start an analysis with raw DNA sequence data and finish with publication-quality figures and statistical results. --- 2016-2021, QIIME 2 development team.

~32,558 citations of QIIME and QIIME2 – Google Scholar, March 2022



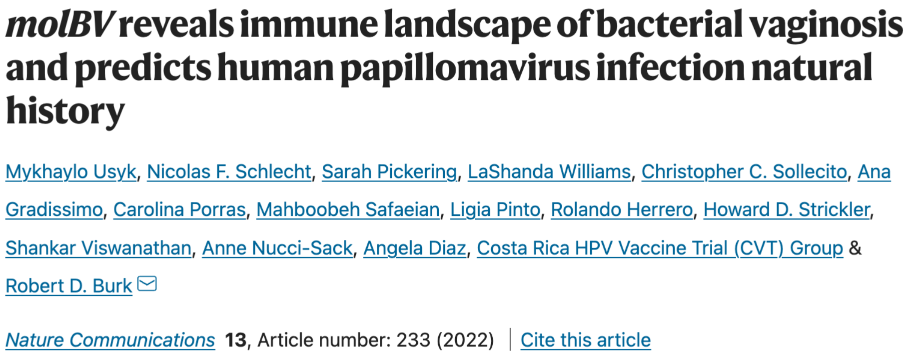
Article | Open Access | Published: 28 September 2021

Gut bacteria identified in colorectal cancer patients promote tumourigenesis via butyrate secretion

Shintaro Okumura, Yusuke Konishi, … Eiji Hara ✉ + Show authors

Nature Communications **12**, Article number: 5674 (2021) | Cite this article

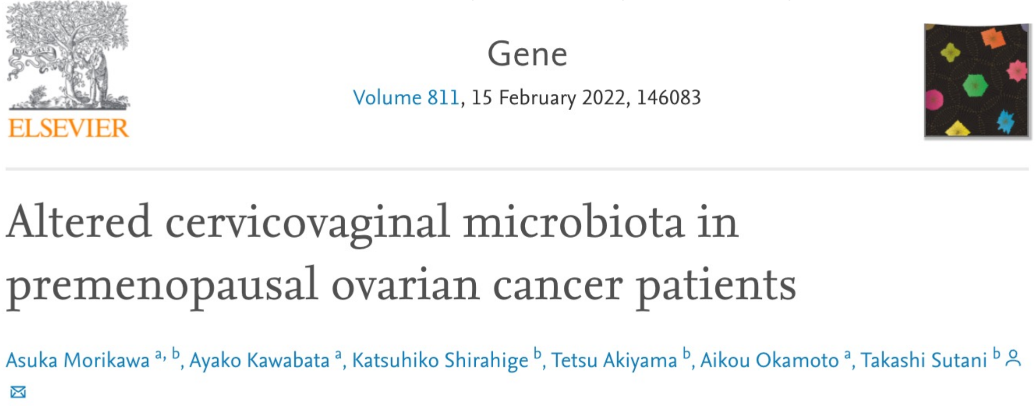
13k Accesses | **9** Citations | **76** Altmetric | Metrics



***molBV* reveals immune landscape of bacterial vaginosis and predicts human papillomavirus infection natural history**

Mykhaylo Usyk, Nicolas F. Schlecht, Sarah Pickering, LaShanda Williams, Christopher C. Sollecito, Ana Gradissimo, Carolina Porras, Mahboobeh Safaeian, Ligia Pinto, Rolando Herrero, Howard D. Strickler, Shankar Viswanathan, Anne Nucci-Sack, Angela Diaz, Costa Rica HPV Vaccine Trial (CVT) Group & Robert D. Burk ✉

Nature Communications **13**, Article number: 233 (2022) | Cite this article



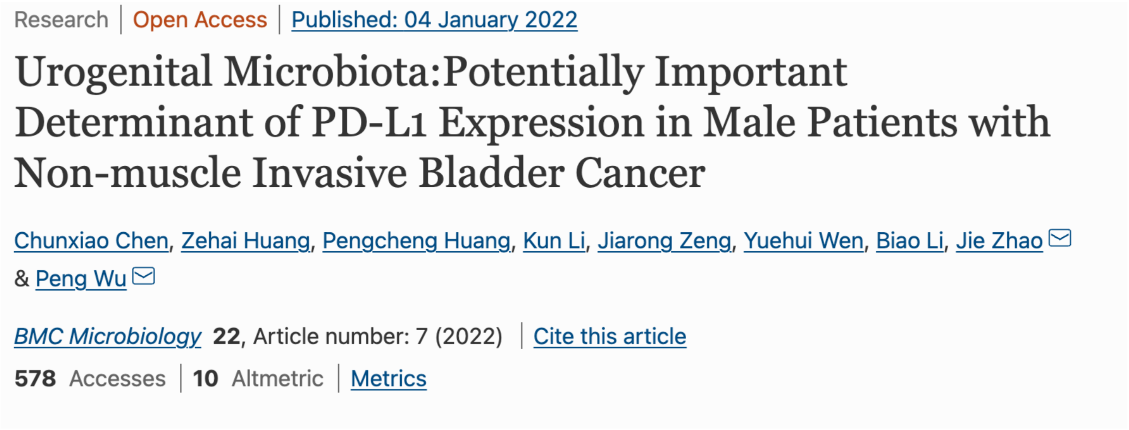
ELSEVIER

Gene

Volume 811, 15 February 2022, 146083

Altered cervicovaginal microbiota in premenopausal ovarian cancer patients

Asuka Morikawa [a, b], Ayako Kawabata [a], Katsuhiko Shirahige [b], Tetsu Akiyama [b], Aikou Okamoto [a], Takashi Sutani [b] ✉



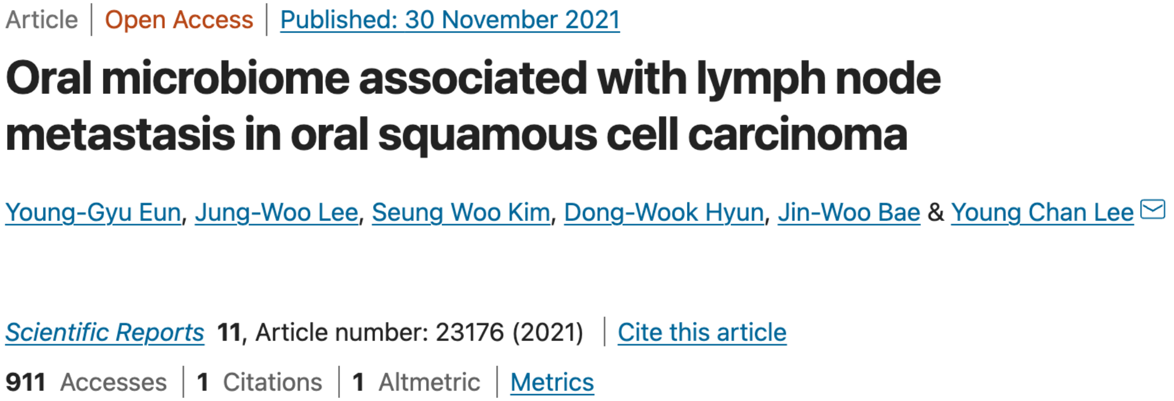
Research | Open Access | Published: 04 January 2022

Urogenital Microbiota:Potentially Important Determinant of PD-L1 Expression in Male Patients with Non-muscle Invasive Bladder Cancer

Chunxiao Chen, Zehai Huang, Pengcheng Huang, Kun Li, Jiarong Zeng, Yuehui Wen, Biao Li, Jie Zhao ✉ & Peng Wu ✉

BMC Microbiology **22**, Article number: 7 (2022) | Cite this article

578 Accesses | **10** Altmetric | Metrics



Article | Open Access | Published: 30 November 2021

Oral microbiome associated with lymph node metastasis in oral squamous cell carcinoma

Young-Gyu Eun, Jung-Woo Lee, Seung Woo Kim, Dong-Wook Hyun, Jin-Woo Bae & Young Chan Lee ✉

Scientific Reports **11**, Article number: 23176 (2021) | Cite this article

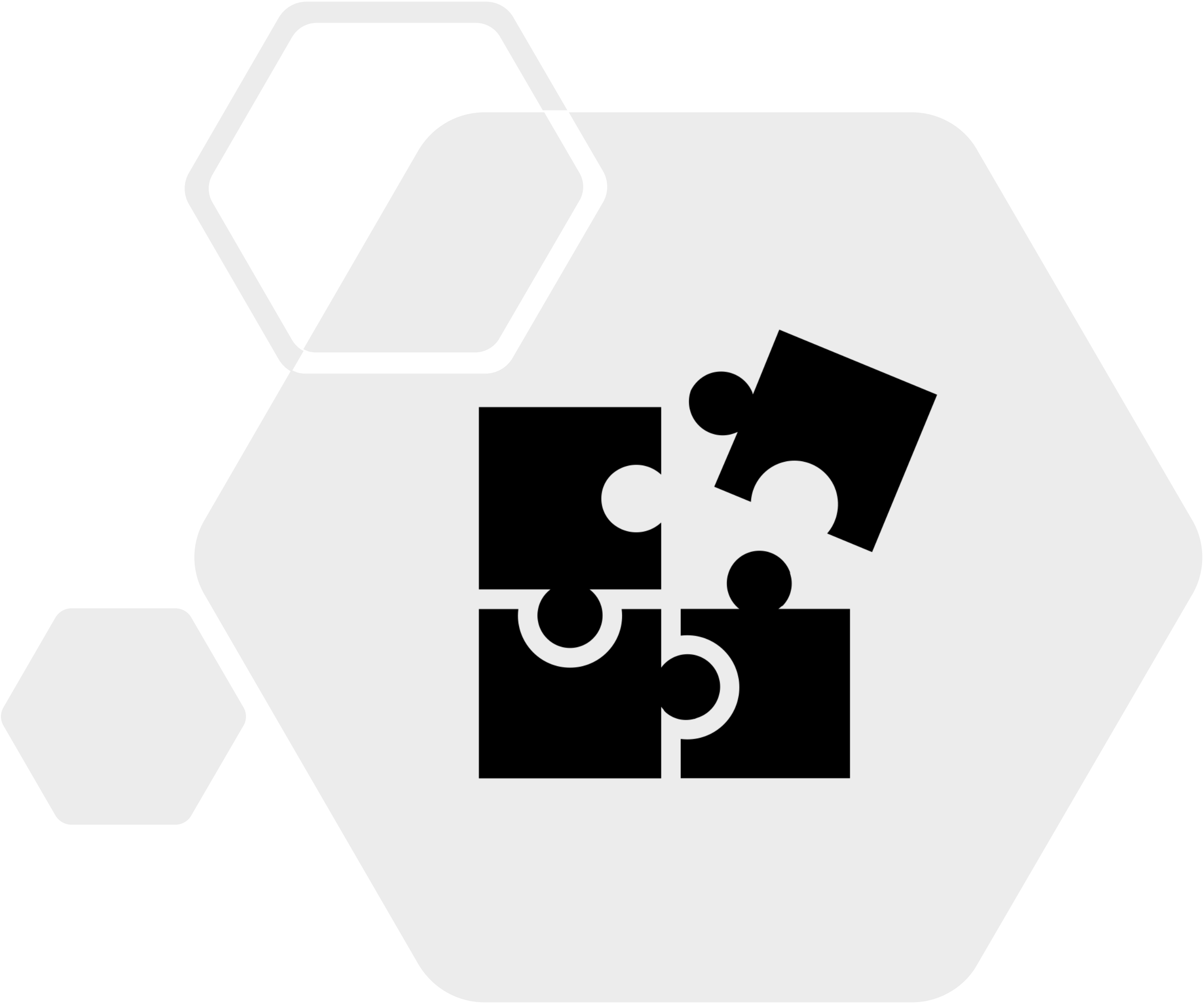
911 Accesses | **1** Citations | **1** Altmetric | Metrics

Why use Qiime2?

- Methods evolve with the field
    - Plug-in architecture
- Interactive data exploration
- Easy to use and accessible
    - Open-source
    - Extensive documentation
    - Tutorials and workshops
- Widespread use
    - Qiime2 forum
    - Global network of collaborators
- Provenance tracking
    - Facilitates reproducibility
- Multiple user interfaces
    - Galaxy
    - Q2 Studio prototype
    - Python API
    - Command line
    - R API (IN THE WORKS)

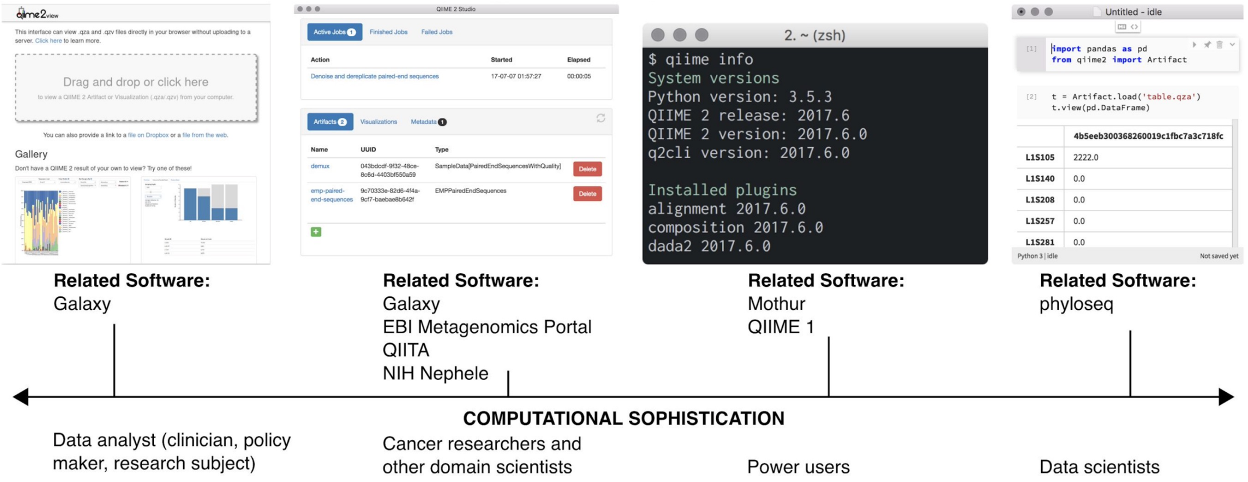
Plug-in Architecture

- Plugins are software packages that can be developed by anyone
- All bioinformatic functionality in QIIME2 defined by plugins
- New plug-ins found in the QIIME2 library



Interfaces

- Q2studio
    - Graphical user interface
- Q2cli
    - Command line interface
    - The classic way to use qiime2
- Artifact API
    - Python 3 application programming interface (API) for QIIME 2
    - Use with Jupyter notebook
    - Recommended for advanced users
- Now on Galaxy
- Potentially coming soon to R
    - For now, qiime2R package



This interface can view .qza and .qzv files directly in your browser without uploading to a server. Click here to learn more.

Drag and drop or click here

to view a QIIME 2 Artifact or Visualization (.qza/.qzv) from your computer.

You can also provide a link to a file on Dropbox or a file from the web.

Gallery

Don't have a QIIME 2 result of your own to view? Try one of these!

Related Software:
Galaxy

Action	Started	Elapsed
Denoise and dereplicate paired-end sequences	17-07-07 01:57:27	00:00:05

Name	UUID	Type	
demux	043bdcdf-9f32-48ce-8c6d-4403bf550a59	SampleData[PairedEndSequencesWithQuality]	Delete
emp-paired-end-sequences	9c70333e-82d6-4f4a-9cf7-baebae8b642f	EMPPairedEndSequences	Delete

Related Software:
Galaxy
EBI Metagenomics Portal
QIITA
NIH Nephele

```
$ qiime info
System versions
Python version: 3.5.3
QIIME 2 release: 2017.6
QIIME 2 version: 2017.6.0
q2cli version: 2017.6.0

Installed plugins
alignment 2017.6.0
composition 2017.6.0
dada2 2017.6.0
```

Related Software:
Mothur
QIIME 1

```
[1]  import pandas as pd
     from qiime2 import Artifact
```

```
[2]  t = Artifact.load('table.qza')
     t.view(pd.DataFrame)
```

	4b5eeb300368260019c1fbc7a3c718fc
L1S105	2222.0
L1S140	0.0
L1S208	0.0
L1S257	0.0
L1S281	0.0

Related Software:
phyloseq

COMPUTATIONAL SOPHISTICATION

Data analyst (clinician, policy maker, research subject)

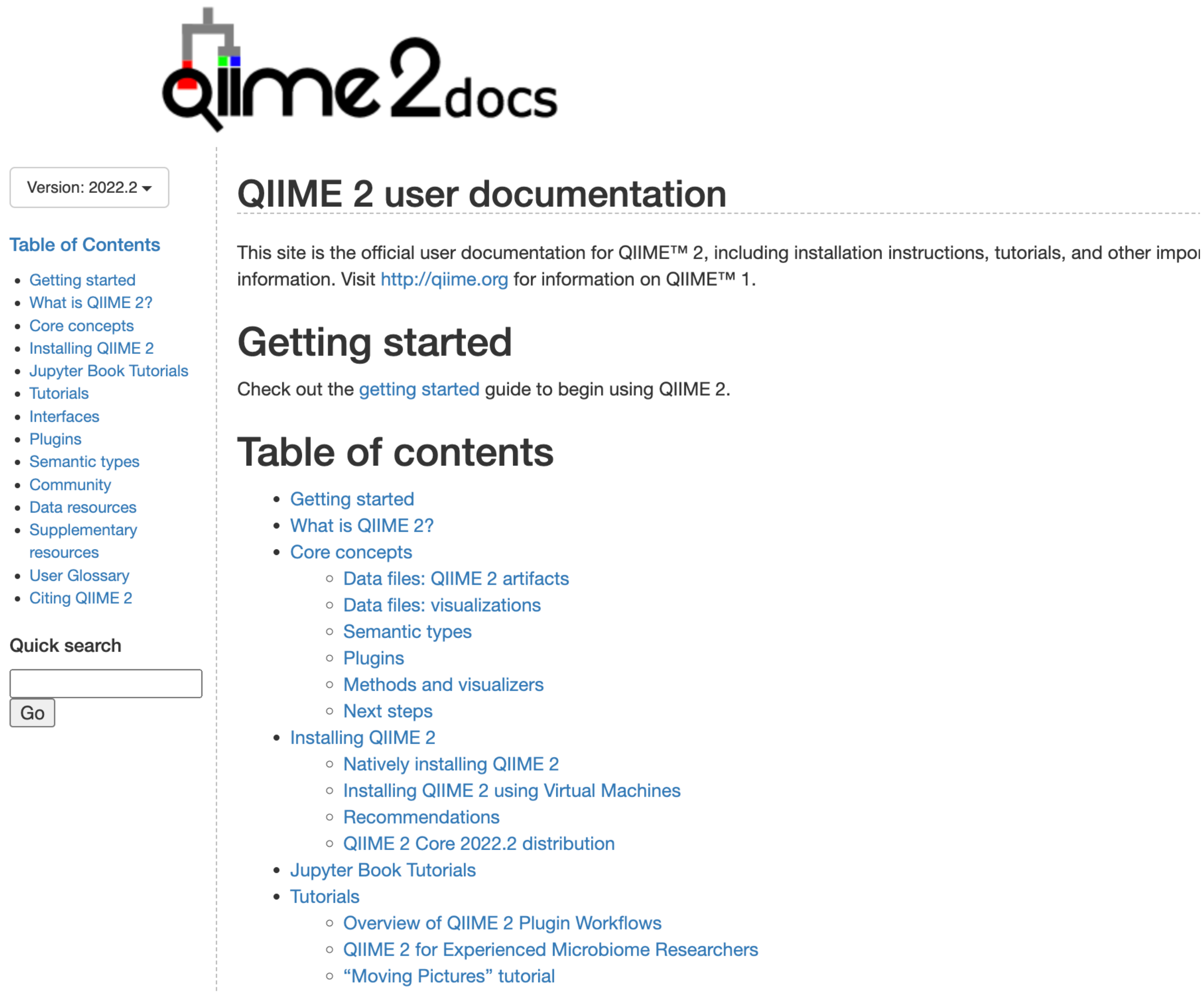
Cancer researchers and other domain scientists

Power users

Data scientists

Qiime2 developers, 2021 workshop content

Qiime2 Documentation



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- Semantic types
- Community
- Data resources
- Supplementary resources
- User Glossary
- Citing QIIME 2

Quick search

QIIME 2 user documentation

This site is the official user documentation for QIIME™ 2, including installation instructions, tutorials, and other impo
information. Visit http://qiime.org for information on QIIME™ 1.

Getting started

Check out the getting started guide to begin using QIIME 2.

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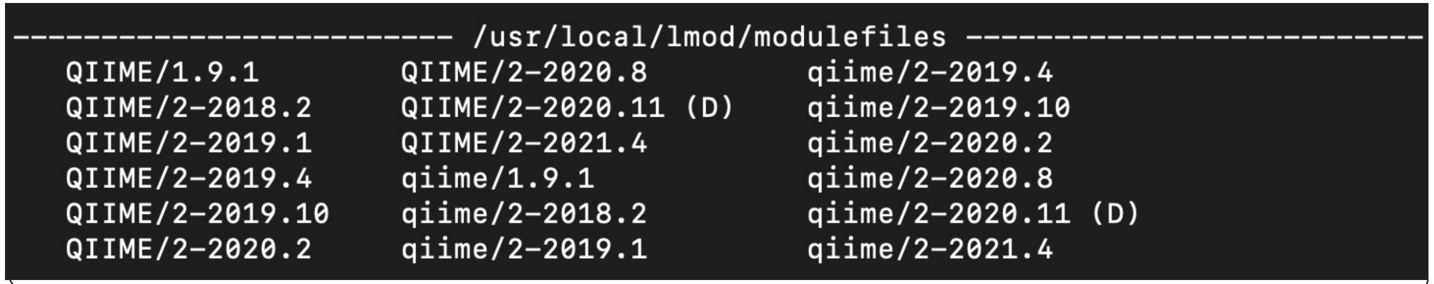
Qiime2 Installation



```
------------------------- /usr/local/lmod/modulefiles -------------------------
   QIIME/1.9.1          QIIME/2-2020.8           qiime/2-2019.4
   QIIME/2-2018.2       QIIME/2-2020.11 (D)      qiime/2-2019.10
   QIIME/2-2019.1       QIIME/2-2021.4           qiime/2-2020.2
   QIIME/2-2019.4       qiime/1.9.1              qiime/2-2020.8
   QIIME/2-2019.10      qiime/2-2018.2           qiime/2-2020.11 (D)
   QIIME/2-2020.2       qiime/2-2019.1           qiime/2-2021.4
```

q2cli installation on macOS, Linux, and Windows (WSL)

Qiime2 installed on Biowulf

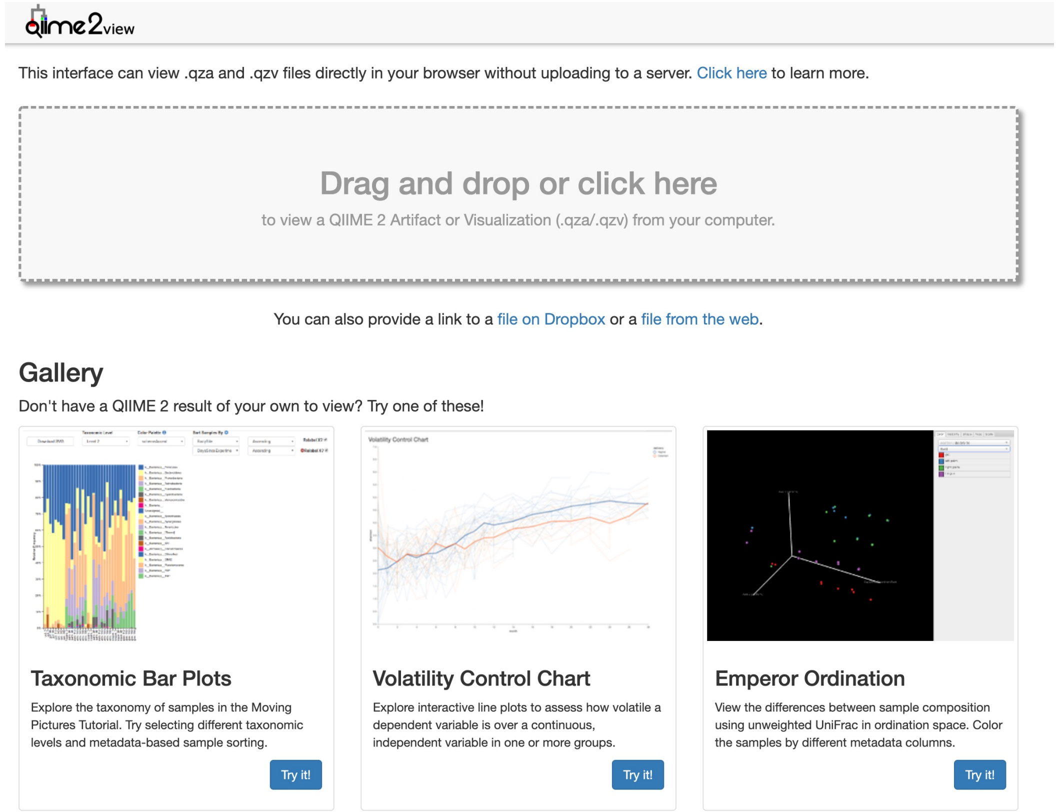
module load QIIME

Getting a Biowulf account:
https://hpc.nih.gov/docs/accounts.html

Qiime 2 Biowulf help page
https://hpc.nih.gov/apps/QIIME.html#:~:text=QIIME2%20on%20Biowulf&text=QIIME%202%20is%20a%20powerful,quality%20figures%20and%20statistical%20results.

Tools for Reproducibility

Qiime2view



This interface can view .qza and .qzv files directly in your browser without uploading to a server. Click here to learn more.

Drag and drop or click here

to view a QIIME 2 Artifact or Visualization (.qza/.qzv) from your computer.

You can also provide a link to a file on Dropbox or a file from the web.

Gallery

Don't have a QIIME 2 result of your own to view? Try one of these!

Taxonomic Bar Plots

Explore the taxonomy of samples in the Moving Pictures Tutorial. Try selecting different taxonomic levels and metadata-based sample sorting.

Try it!

Volatility Control Chart

Explore interactive line plots to assess how volatile a dependent variable is over a continuous, independent variable in one or more groups.

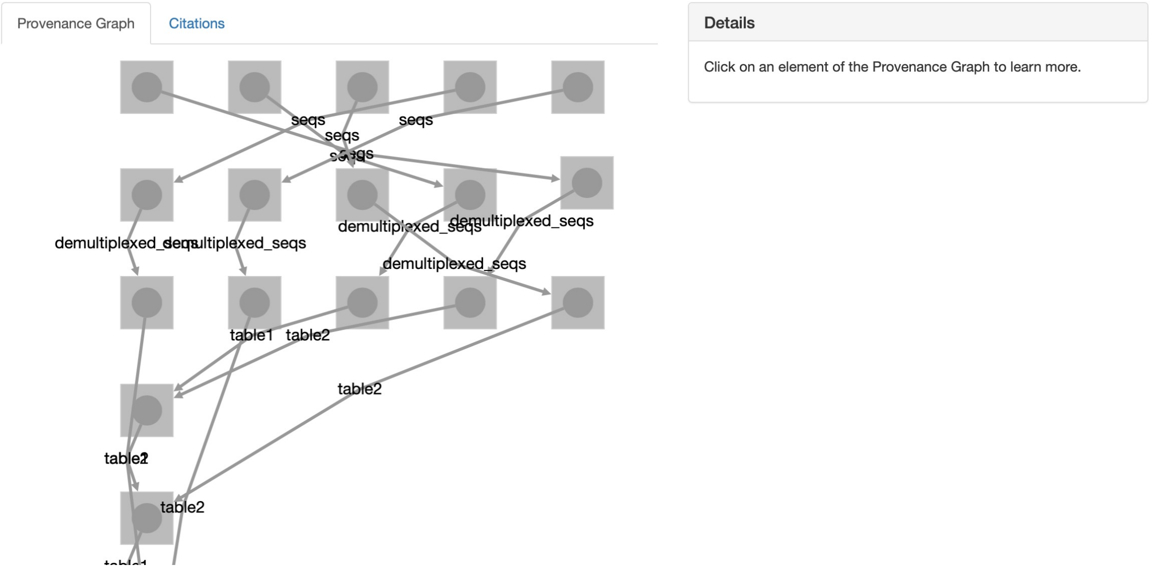
Try it!

Emperor Ordination

View the differences between sample composition using unweighted UniFrac in ordination space. Color the samples by different metadata columns.

Try it!

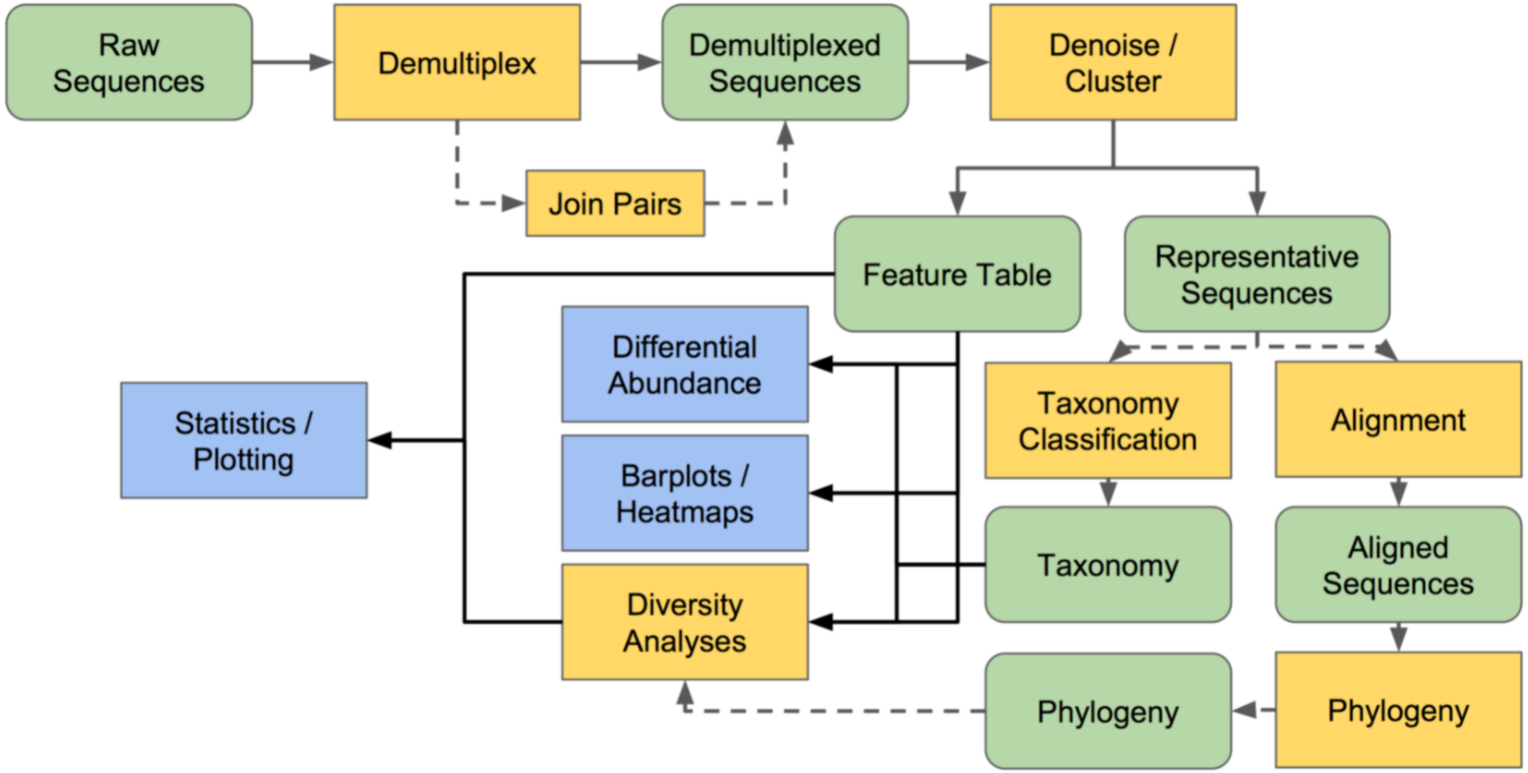
Provenance Tracking



Details

Click on an element of the Provenance Graph to learn more.

Q2 workflows



https://docs.qiime2.org/2022.2/tutorials/overview/#let-s-get-oriented-flowcharts

Core plug-in Overview

https://docs.qiime2.org/2022.2/plugins/available/

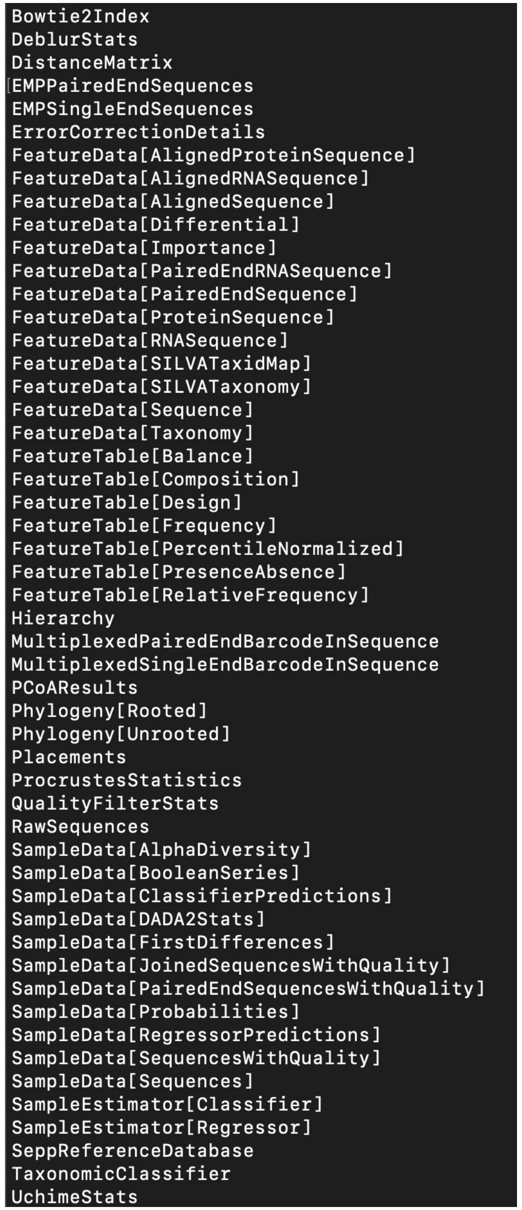
Available plugins and methods with q2 installation

- Focus on amplicon sequence processing and analysis
  - Primary targets: 16S rRNA, 18S rRNA, ITS
    - QC analysis, adapter / primer trimming via cutadapt
    - OTU clustering, Sequence Denoising
      - DADA2, Deblur, OTU clustering via vsearch (close reference and open reference)
    - Taxonomic Classification
    - Tree building
      - MAFT and fasttree
      - Raxml
      - SEPP fragment insertion
    - Data analysis
      - RF classification, differential abundance testing, core features, alpha diversity, beta diversity, longitudinal methods.

Data import types

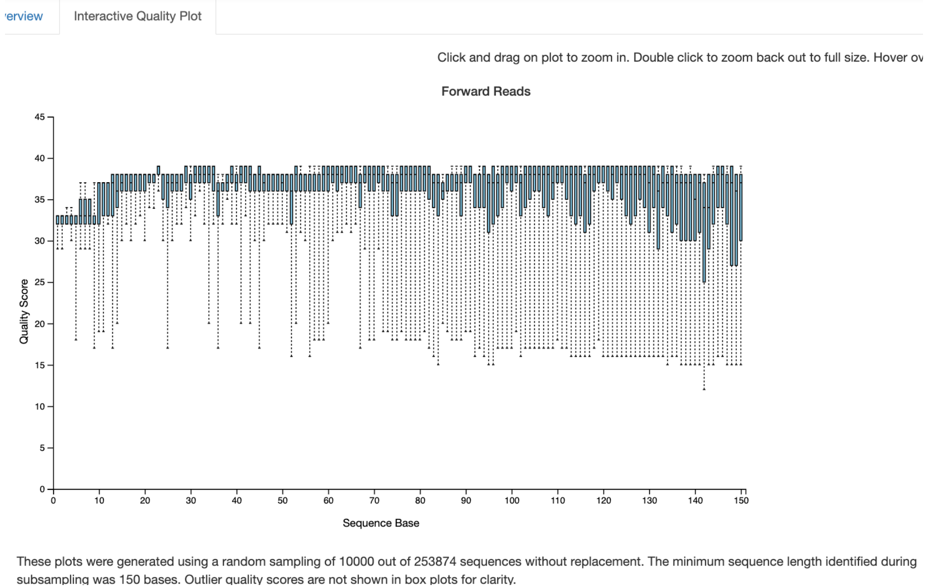
- First step = data import
  - Can import at most stages in the analysis
    - qiime tools import –h
  - Raw data usually some type of fastq files
    - EMPPairedEndSequences
    - EMPSingleEndSequences
    - SampleData[SequencesWithQuality]
    - MultiplexedPairedEndBarcodeInSequence
    - RawSequences
- See the import tutorial for help
  - https://docs.qiime2.org/2022.2/tutorials/importing/

```
qiime tools import --show-importable-types
```



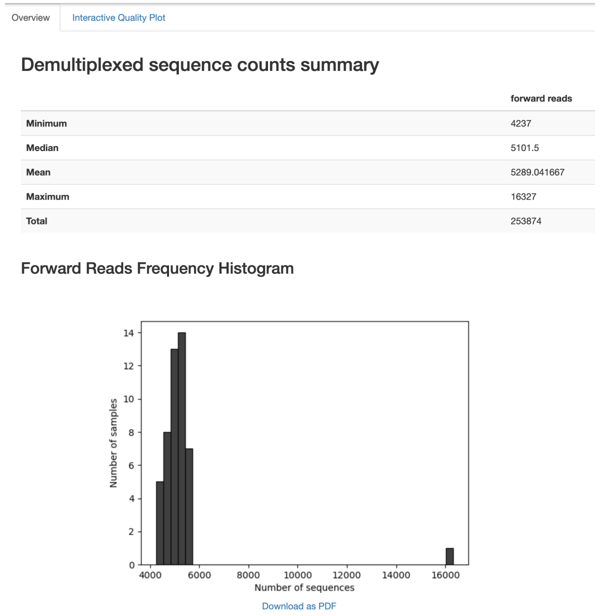
```
Bowtie2Index
DeblurStats
DistanceMatrix
EMPPairedEndSequences
EMPSingleEndSequences
ErrorCorrectionDetails
FeatureData[AlignedProteinSequence]
FeatureData[AlignedRNASequence]
FeatureData[AlignedSequence]
FeatureData[Differential]
FeatureData[Importance]
FeatureData[PairedEndRNASequence]
FeatureData[PairedEndSequence]
FeatureData[ProteinSequence]
FeatureData[RNASequence]
FeatureData[SILVATaxidMap]
FeatureData[SILVATaxonomy]
FeatureData[Sequence]
FeatureData[Taxonomy]
FeatureTable[Balance]
FeatureTable[Composition]
FeatureTable[Design]
FeatureTable[Frequency]
FeatureTable[PercentileNormalized]
FeatureTable[PresenceAbsence]
FeatureTable[RelativeFrequency]
Hierarchy
MultiplexedPairedEndBarcodeInSequence
MultiplexedSingleEndBarcodeInSequence
PCoAResults
Phylogeny[Rooted]
Phylogeny[Unrooted]
Placements
ProcrustesStatistics
QualityFilterStats
RawSequences
SampleData[AlphaDiversity]
SampleData[BooleanSeries]
SampleData[ClassifierPredictions]
SampleData[DADA2Stats]
SampleData[FirstDifferences]
SampleData[JoinedSequencesWithQuality]
SampleData[PairedEndSequencesWithQuality]
SampleData[Probabilities]
SampleData[RegressorPredictions]
SampleData[SequencesWithQuality]
SampleData[Sequences]
SampleEstimator[Classifier]
SampleEstimator[Regressor]
SeppReferenceDatabase
TaxonomicClassifier
UchimeStats
```

Demultiplex methods & Quality Control



Click and drag on plot to zoom in. Double click to zoom back out to full size. Hover ov

These plots were generated using a random sampling of 10000 out of 253874 sequences without replacement. The minimum sequence length identified during subsampling was 150 bases. Outlier quality scores are not shown in box plots for clarity.



Demultiplexed sequence counts summary

	forward reads
Minimum	4237
Median	5101.5
Mean	5289.041667
Maximum	16327
Total	253874

Forward Reads Frequency Histogram

Demultiplex: Associating sequences with samples

- May be done by the sequencing core
- Methods available
    - q2-demux
        - Emp-paired
        - Emp-single
    - q2-cutadapt
        - Demux-paired
        - Demux-single

Quality Control

- Adapter, primer trimming
    - Q2-cutadapt
- Quality score filtering
    - q2-quality-filter
- Removing human contamination
    - Q2-exclude-seqs
    - Q2-filter-reads
- Community evaluation (expected vs observed)
    - Q2- quality-control

Feature Table generation

- OTU clustering
  - vsearch
- Denoising
  - Deblur
  - DADA2

Outputs: Two key files

1. Feature table
2. Representative Sequences

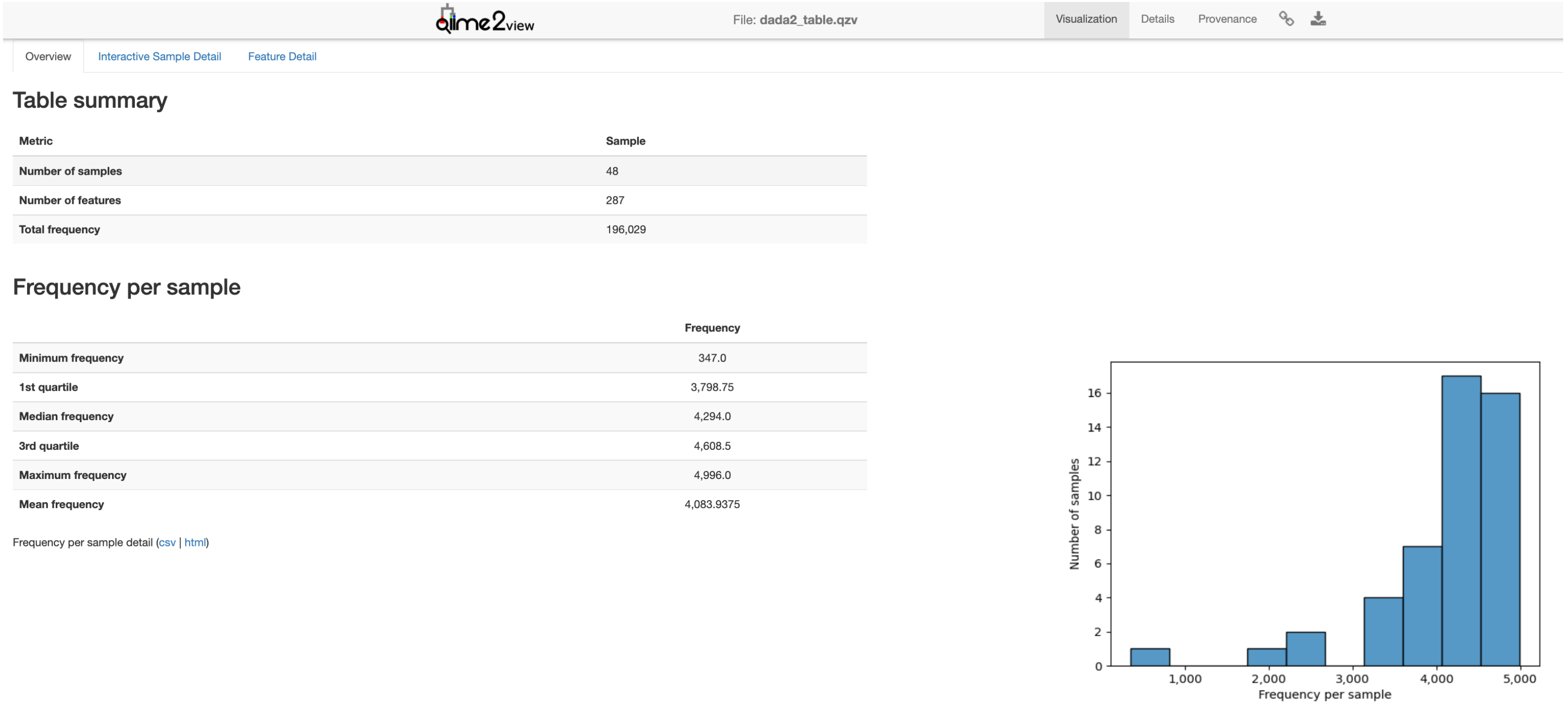


Table summary

Metric	Sample
Number of samples	48
Number of features	287
Total frequency	196,029

Frequency per sample

	Frequency
Minimum frequency	347.0
1st quartile	3,798.75
Median frequency	4,294.0
3rd quartile	4,608.5
Maximum frequency	4,996.0
Mean frequency	4,083.9375

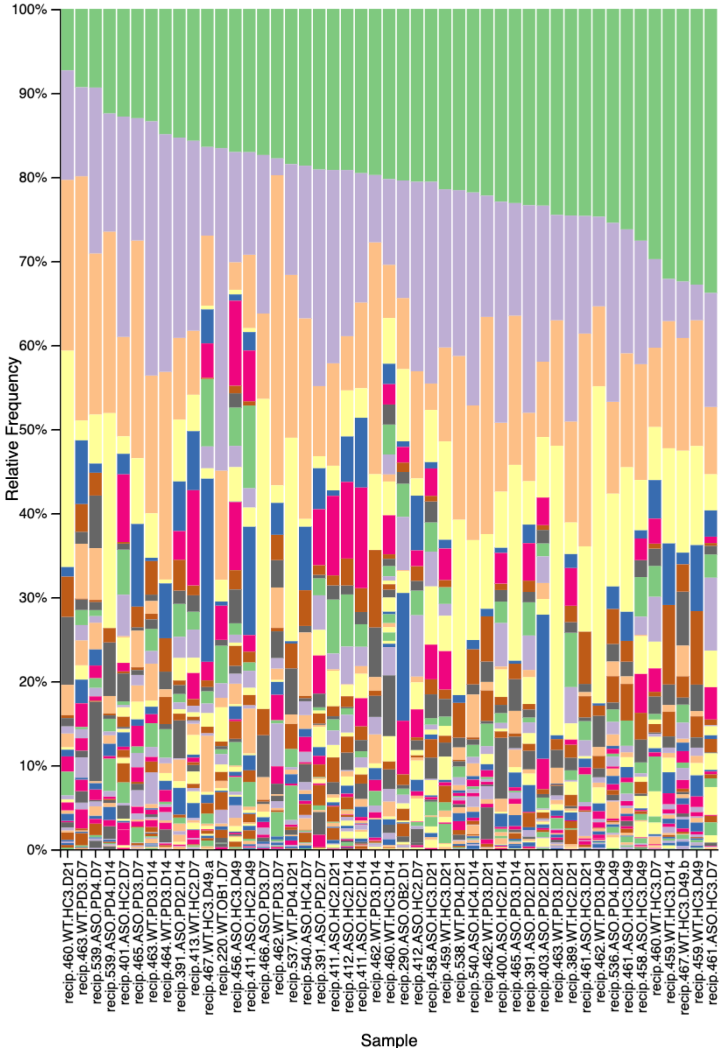
Frequency per sample detail (csv | html)

Other feature table methods:
https://docs.qiime2.org/2022.2/plugins/available/feature-table/

Taxonomic Classification & Phylogenetic Tree

Taxonomy

- classify-consensus-blast
  - BLAST+ consensus taxonomy classifier
- classify-consensus-vsearch
  - VSEARCH-based consensus taxonomy classifier
- classify-sklearn
  - Pre-fitted sklearn-based taxonomy classifier



Tree

- Fragment insertion – SEPP
- qiime phylogeny
  - align-to-tree-mafft-fasttree
  - align-to-tree-mafft-iqtree
  - align-to-tree-mafft-raxml

NO CURRENT WAY TO VIEW TREES USING QIIME2 PLATFORM

Community analysis (visualizations / statistics)

qiime diversity core-metrics-phylogenetic

- Emperor plots

Alpha and beta group significance testing

- output

Differential abundance testing

- ANCOM

Longitudinal testing

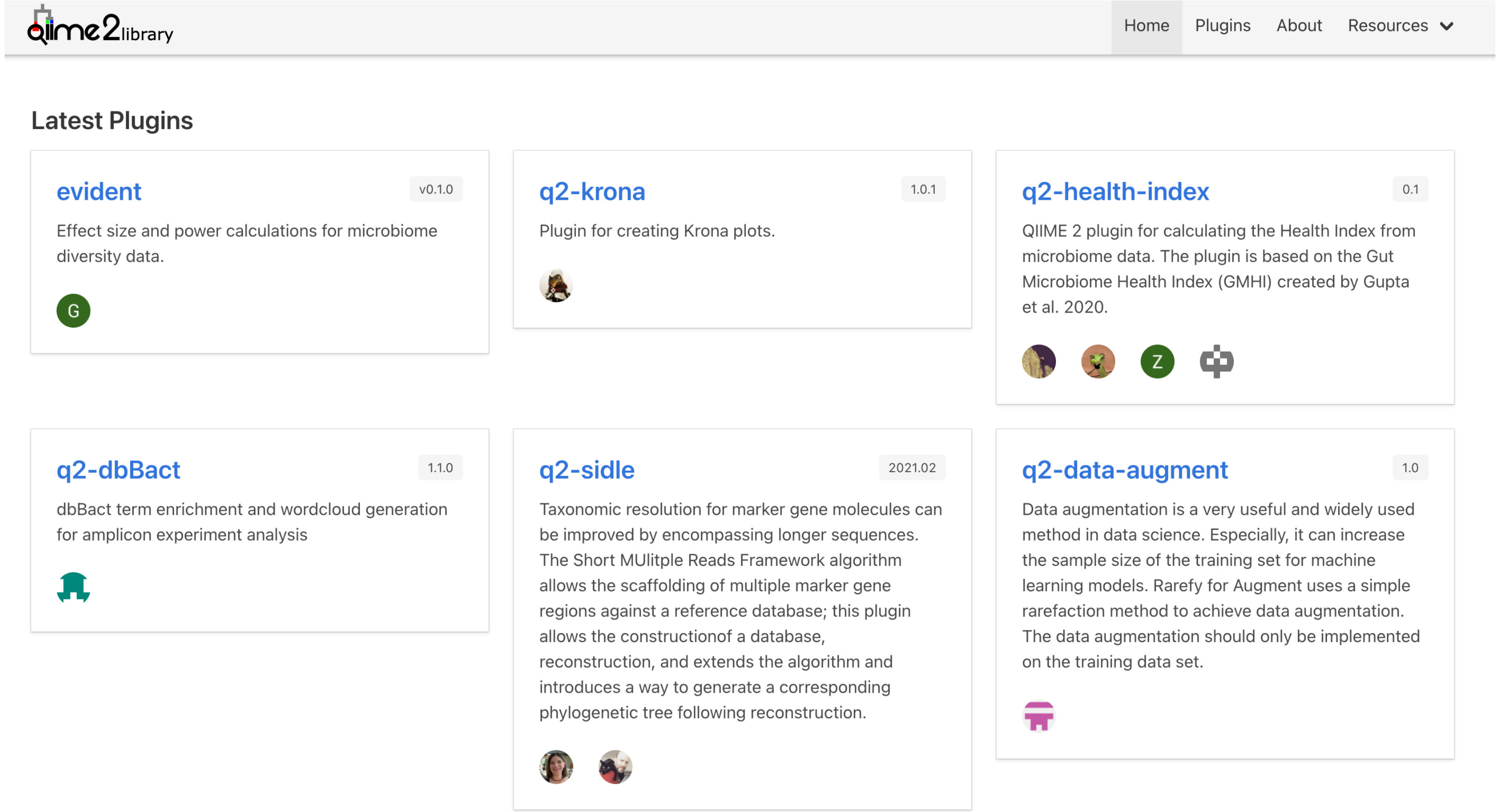
- Distance based

Data Resources

- Taxonomy Classifiers
- Weighted Taxonomic Classifiers
- Q2 formatted reference marker gene databases
- SEPP reference databases

https://docs.qiime2.org/2022.2/data-resources/

QIIME2 Plugin Library



Latest Plugins

evident v0.1.0

Effect size and power calculations for microbiome diversity data.

q2-krona 1.0.1

Plugin for creating Krona plots.

q2-health-index 0.1

QIIME 2 plugin for calculating the Health Index from microbiome data. The plugin is based on the Gut Microbiome Health Index (GMHI) created by Gupta et al. 2020.

q2-dbBact 1.1.0

dbBact term enrichment and wordcloud generation for amplicon experiment analysis

q2-sidle 2021.02

Taxonomic resolution for marker gene molecules can be improved by encompassing longer sequences. The Short MUlitple Reads Framework algorithm allows the scaffolding of multiple marker gene regions against a reference database; this plugin allows the constructionof a database, reconstruction, and extends the algorithm and introduces a way to generate a corresponding phylogenetic tree following reconstruction.

q2-data-augment 1.0

Data augmentation is a very useful and widely used method in data science. Especially, it can increase the sample size of the training set for machine learning models. Rarefy for Augment uses a simple rarefaction method to achieve data augmentation. The data augmentation should only be implemented on the training data set.

Future Features

- Funding through NCI
  - **To increase the accessibility of the QIIME 2 platform and cancer microbiome data to the cancer research community**
    - Galaxy
    - R API
    - Cancer microbiome data resource via QIITA
    - cancer-focused QIIME 2 user workshop series
    - Collaboration with NCI Cloud Resources teams to integrate QIIME 2
      - Work directly with data from GATK and TCGA
  - **Make QIIME 2 a microbiome mutli-omics bioinformatics platform**
  - **Facilitate reproducible research**

Informatics Technology for Cancer Research program
Project 1U24CA248454-01;
https://reporter.nih.gov/project-details/9951750

Future – omics tools

- Integrating multi-omics data
  - Shotgun surveys of phage and other viruses
  - Functional potential via shotgun metagenomics
  - Functional activity
    - Metatransciptome
    - Metaproteome
    - metabolome

Provenance Replay

- The ability to generate executable workflows from an existing artifact or visualization’s data provenance

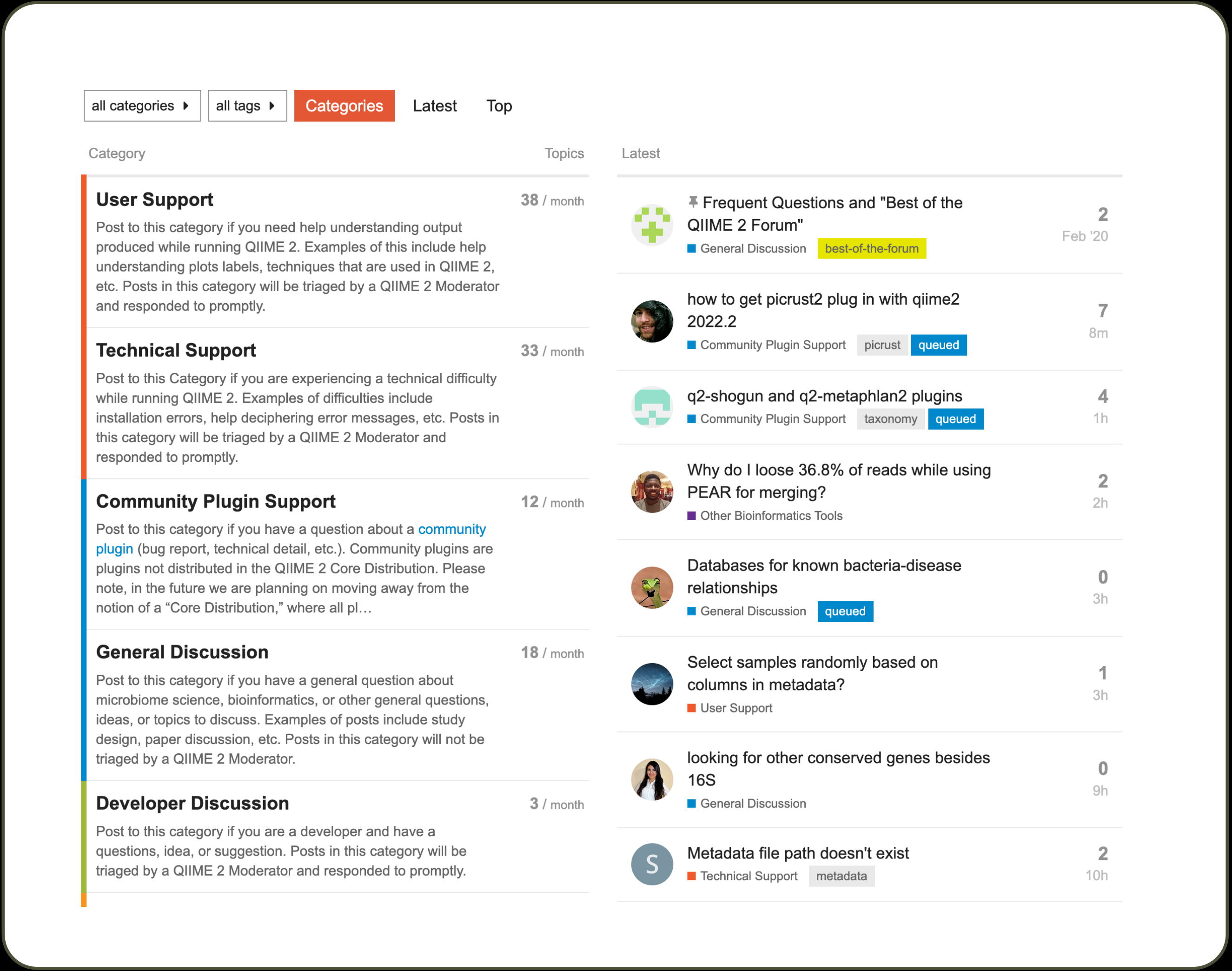
Other features:

- ability to obtain provenance info in a publication ready format
- Automated workflow bug detection from data provenance
- Plugins to help users submit data to repositories

Qiime2 forum

A vast network of collaborators and users

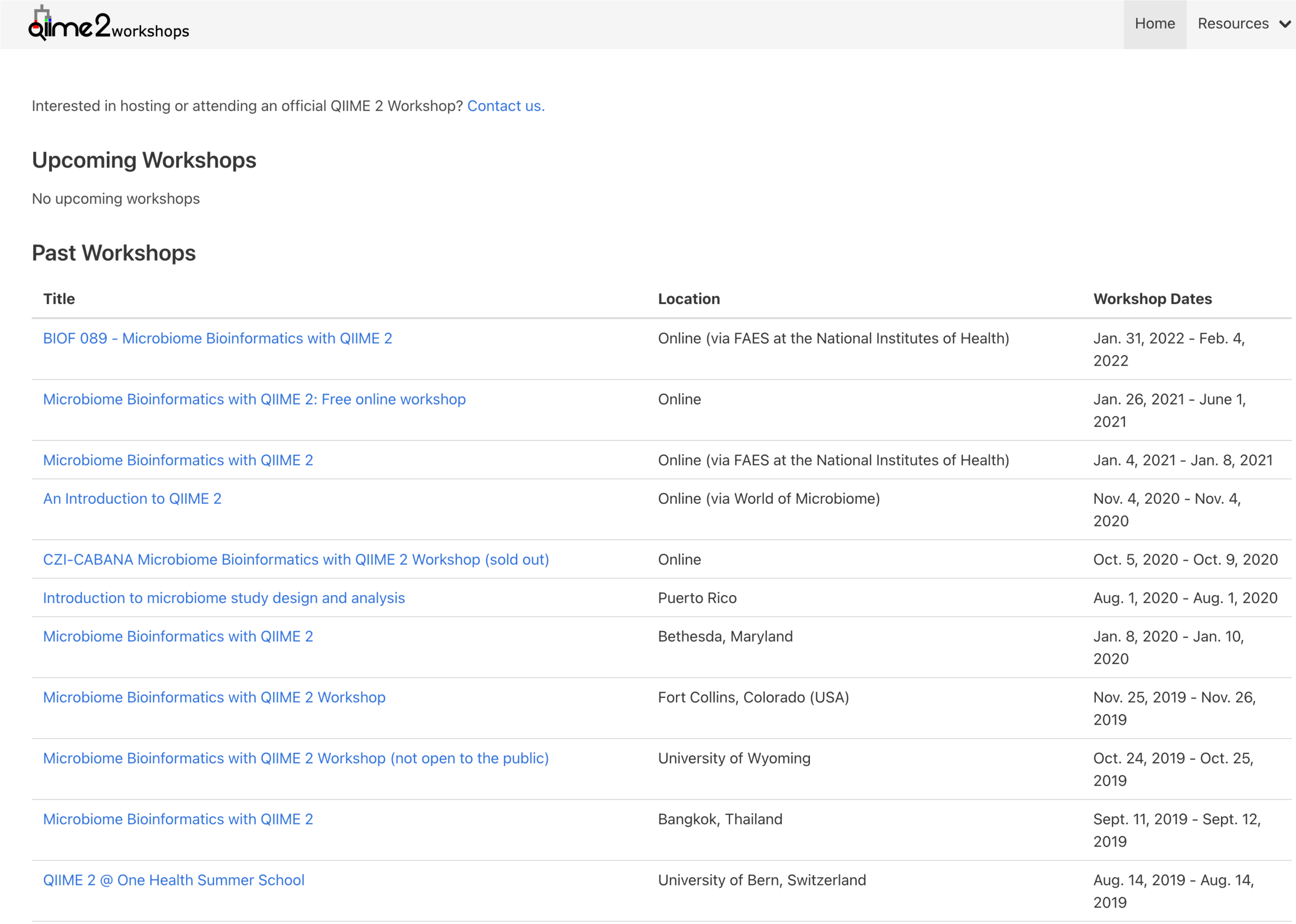
Help in just a short period of time



Category	Topics
User Support Post to this category if you need help understanding output produced while running QIIME 2. Examples of this include help understanding plots labels, techniques that are used in QIIME 2, etc. Posts in this category will be triaged by a QIIME 2 Moderator and responded to promptly.	38 / month
Technical Support Post to this Category if you are experiencing a technical difficulty while running QIIME 2. Examples of difficulties include installation errors, help deciphering error messages, etc. Posts in this category will be triaged by a QIIME 2 Moderator and responded to promptly.	33 / month
Community Plugin Support Post to this category if you have a question about a community plugin (bug report, technical detail, etc.). Community plugins are plugins not distributed in the QIIME 2 Core Distribution. Please note, in the future we are planning on moving away from the notion of a “Core Distribution,” where all pl…	12 / month
General Discussion Post to this category if you have a general question about microbiome science, bioinformatics, or other general questions, ideas, or topics to discuss. Examples of posts include study design, paper discussion, etc. Posts in this category will not be triaged by a QIIME 2 Moderator.	18 / month
Developer Discussion Post to this category if you are a developer and have a questions, idea, or suggestion. Posts in this category will be triaged by a QIIME 2 Moderator and responded to promptly.	3 / month

Latest		
Frequent Questions and "Best of the QIIME 2 Forum" General Discussion best-of-the-forum	2	Feb '20
how to get picrust2 plug in with qiime2 2022.2 Community Plugin Support picrust queued	7	8m
q2-shogun and q2-metaphlan2 plugins Community Plugin Support taxonomy queued	4	1h
Why do I loose 36.8% of reads while using PEAR for merging? Other Bioinformatics Tools	2	2h
Databases for known bacteria-disease relationships General Discussion queued	0	3h
Select samples randomly based on columns in metadata? User Support	1	3h
looking for other conserved genes besides 16S General Discussion	0	9h
Metadata file path doesn't exist Technical Support metadata	2	10h

Current Learning Opportunities through Qiime2



Interested in hosting or attending an official QIIME 2 Workshop? Contact us.

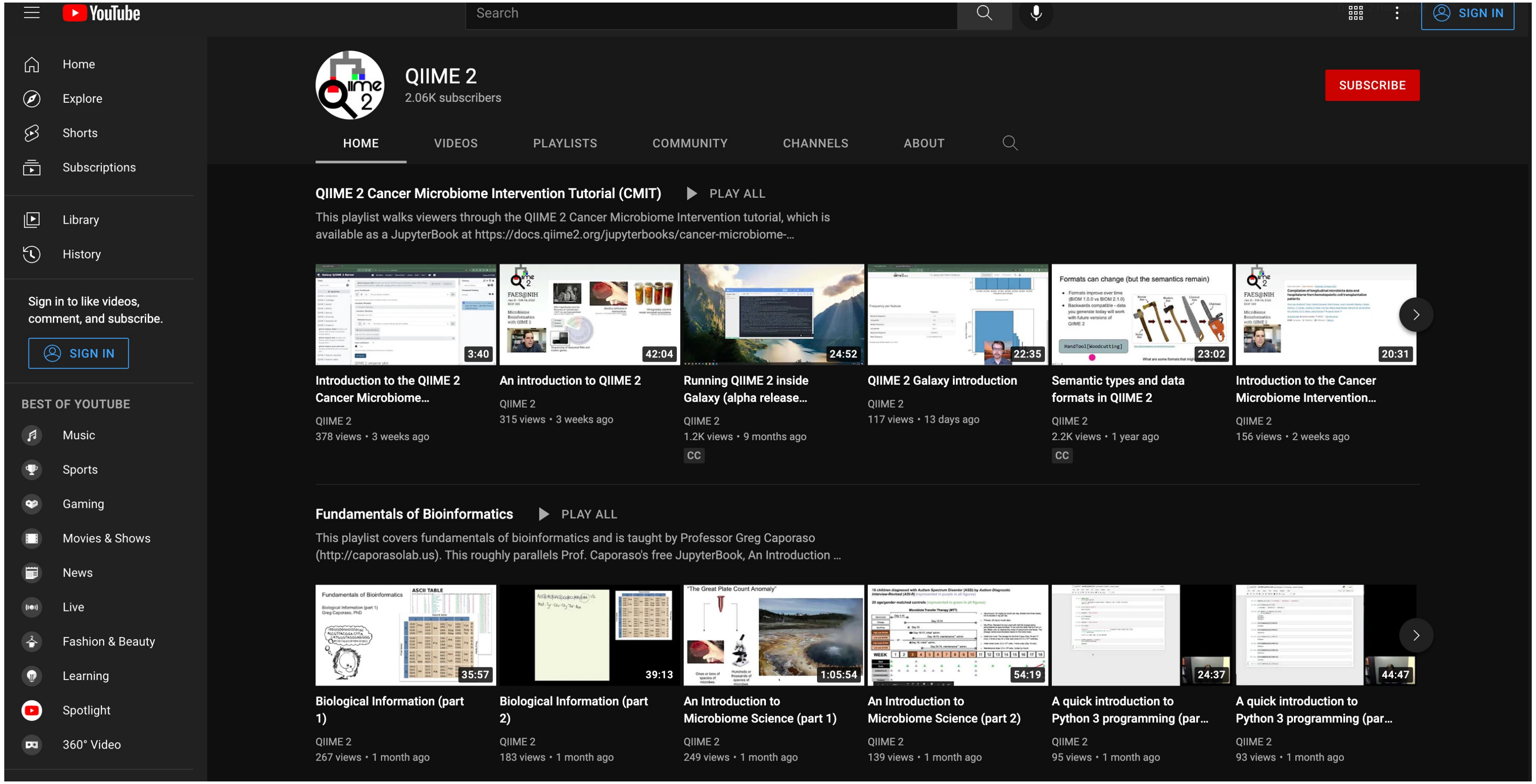
Upcoming Workshops

No upcoming workshops

Past Workshops

Title	Location	Workshop Dates
BIOF 089 - Microbiome Bioinformatics with QIIME 2	Online (via FAES at the National Institutes of Health)	Jan. 31, 2022 - Feb. 4, 2022
Microbiome Bioinformatics with QIIME 2: Free online workshop	Online	Jan. 26, 2021 - June 1, 2021
Microbiome Bioinformatics with QIIME 2	Online (via FAES at the National Institutes of Health)	Jan. 4, 2021 - Jan. 8, 2021
An Introduction to QIIME 2	Online (via World of Microbiome)	Nov. 4, 2020 - Nov. 4, 2020
CZI-CABANA Microbiome Bioinformatics with QIIME 2 Workshop (sold out)	Online	Oct. 5, 2020 - Oct. 9, 2020
Introduction to microbiome study design and analysis	Puerto Rico	Aug. 1, 2020 - Aug. 1, 2020
Microbiome Bioinformatics with QIIME 2	Bethesda, Maryland	Jan. 8, 2020 - Jan. 10, 2020
Microbiome Bioinformatics with QIIME 2 Workshop	Fort Collins, Colorado (USA)	Nov. 25, 2019 - Nov. 26, 2019
Microbiome Bioinformatics with QIIME 2 Workshop (not open to the public)	University of Wyoming	Oct. 24, 2019 - Oct. 25, 2019
Microbiome Bioinformatics with QIIME 2	Bangkok, Thailand	Sept. 11, 2019 - Sept. 12, 2019
QIIME 2 @ One Health Summer School	University of Bern, Switzerland	Aug. 14, 2019 - Aug. 14, 2019

QIIME2 Youtube Channel



Sign in to like videos, comment, and subscribe.

QIIME 2
2.06K subscribers

QIIME 2 Cancer Microbiome Intervention Tutorial (CMIT)

This playlist walks viewers through the QIIME 2 Cancer Microbiome Intervention tutorial, which is available as a JupyterBook at https://docs.qiime2.org/jupyterbooks/cancer-microbiome-...

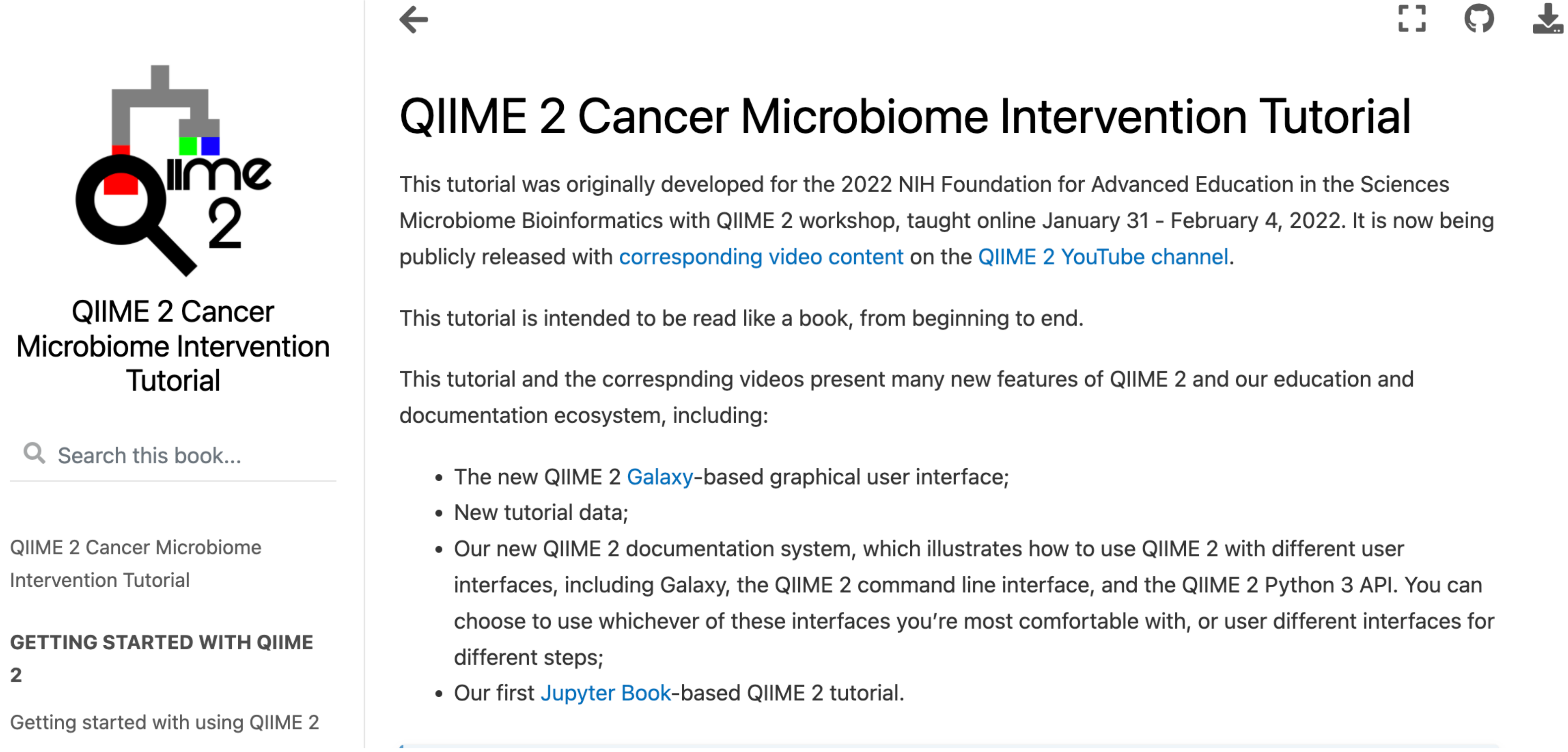
Video	Length	Channel	Views
Introduction to the QIIME 2 Cancer Microbiome...	3:40	QIIME 2	378 views • 3 weeks ago
An introduction to QIIME 2	42:04	QIIME 2	315 views • 3 weeks ago
Running QIIME 2 inside Galaxy (alpha release...	24:52	QIIME 2	1.2K views • 9 months ago
QIIME 2 Galaxy introduction	22:35	QIIME 2	117 views • 13 days ago
Semantic types and data formats in QIIME 2	23:02	QIIME 2	2.2K views • 1 year ago
Introduction to the Cancer Microbiome Intervention...	20:31	QIIME 2	156 views • 2 weeks ago

Fundamentals of Bioinformatics

This playlist covers fundamentals of bioinformatics and is taught by Professor Greg Caporaso (http://caporasolab.us). This roughly parallels Prof. Caporaso's free JupyterBook, An Introduction ...

Video	Length	Channel	Views
Biological Information (part 1)	35:57	QIIME 2	267 views • 1 month ago
Biological Information (part 2)	39:13	QIIME 2	183 views • 1 month ago
An Introduction to Microbiome Science (part 1)	1:05:54	QIIME 2	249 views • 1 month ago
An Introduction to Microbiome Science (part 2)	54:19	QIIME 2	139 views • 1 month ago
A quick introduction to Python 3 programming (par...	24:37	QIIME 2	95 views • 1 month ago
A quick introduction to Python 3 programming (par...	44:47	QIIME 2	93 views • 1 month ago

New Cancer Microbiome Tutorial using Galaxy!



QIIME 2 Cancer Microbiome Intervention Tutorial

Search this book...

QIIME 2 Cancer Microbiome Intervention Tutorial

GETTING STARTED WITH QIIME 2

Getting started with using QIIME 2

QIIME 2 Cancer Microbiome Intervention Tutorial

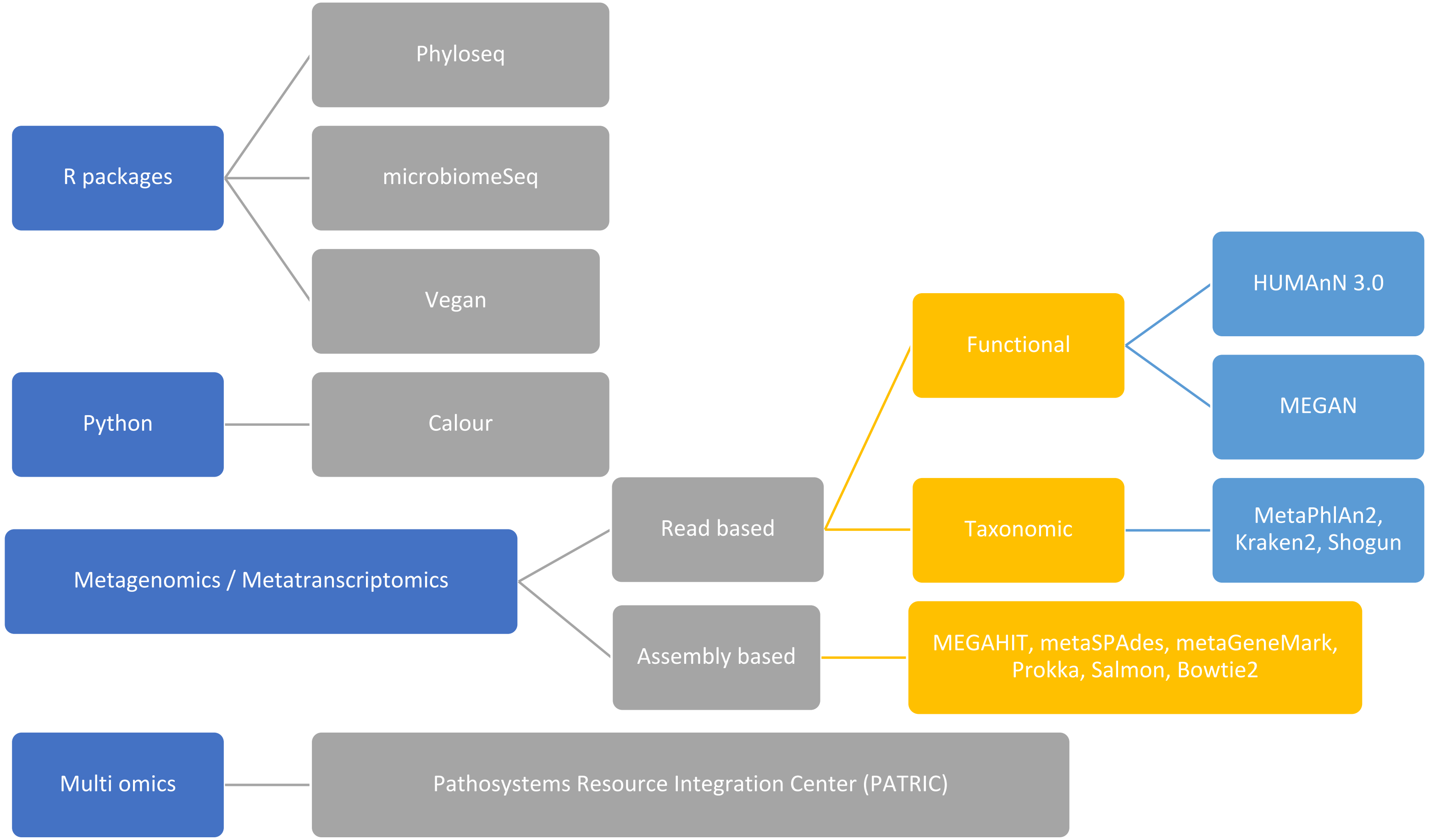
This tutorial was originally developed for the 2022 NIH Foundation for Advanced Education in the Sciences Microbiome Bioinformatics with QIIME 2 workshop, taught online January 31 - February 4, 2022. It is now being publicly released with corresponding video content on the QIIME 2 YouTube channel.

This tutorial is intended to be read like a book, from beginning to end.

This tutorial and the correspnding videos present many new features of QIIME 2 and our education and documentation ecosystem, including:

- The new QIIME 2 Galaxy-based graphical user interface;
- New tutorial data;
- Our new QIIME 2 documentation system, which illustrates how to use QIIME 2 with different user interfaces, including Galaxy, the QIIME 2 command line interface, and the QIIME 2 Python 3 API. You can choose to use whichever of these interfaces you're most comfortable with, or user different interfaces for different steps;
- Our first Jupyter Book-based QIIME 2 tutorial.

Going beyond qiime2



- R packages
  - Phyloseq
  - microbiomeSeq
  - Vegan
- Python
  - Calour
- Metagenomics / Metatranscriptomics
  - Read based
    - Functional
      - HUMAnN 3.0
      - MEGAN
    - Taxonomic
      - MetaPhlAn2, Kraken2, Shogun
  - Assembly based
    - MEGAHIT, metaSPAdes, metaGeneMark, Prokka, Salmon, Bowtie2
- Multi omics
  - Pathosystems Resource Integration Center (PATRIC)

Contact me at ncibtep@nih.gov for help regarding this resource.